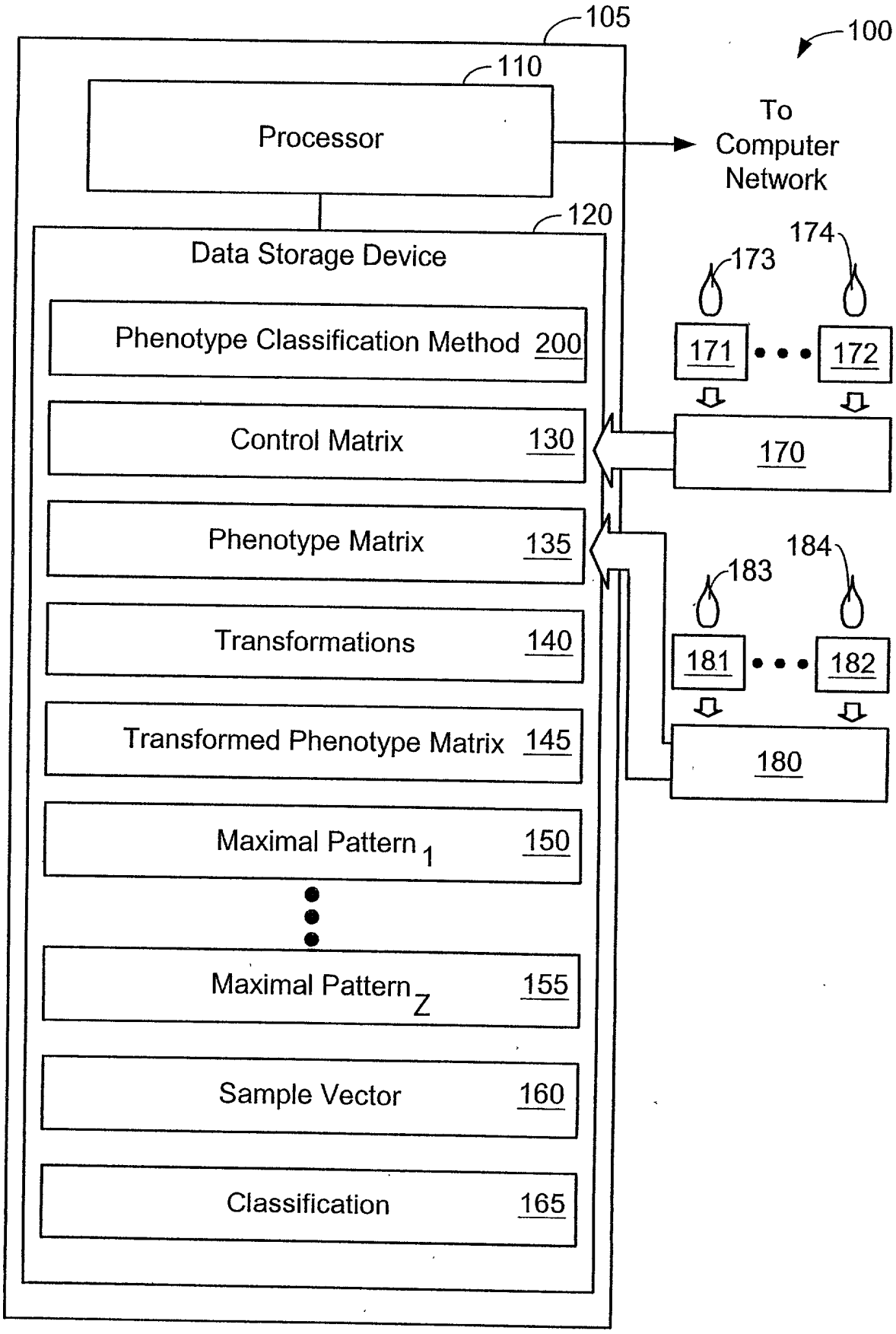
105
100
110
Processor
To
Computer
Network
120
Data Storage Device
174
173
171
172
Phenotype Classification Method 200
Control Matrix 130
170
Phenotype Matrix 135
184
183
181
182
Transformations 140
Transformed Phenotype Matrix 145
180
Maximal Pattern 1 150
Maximal Pattern Z 155
Sample Vector 160
Classification 165

FIG. 1

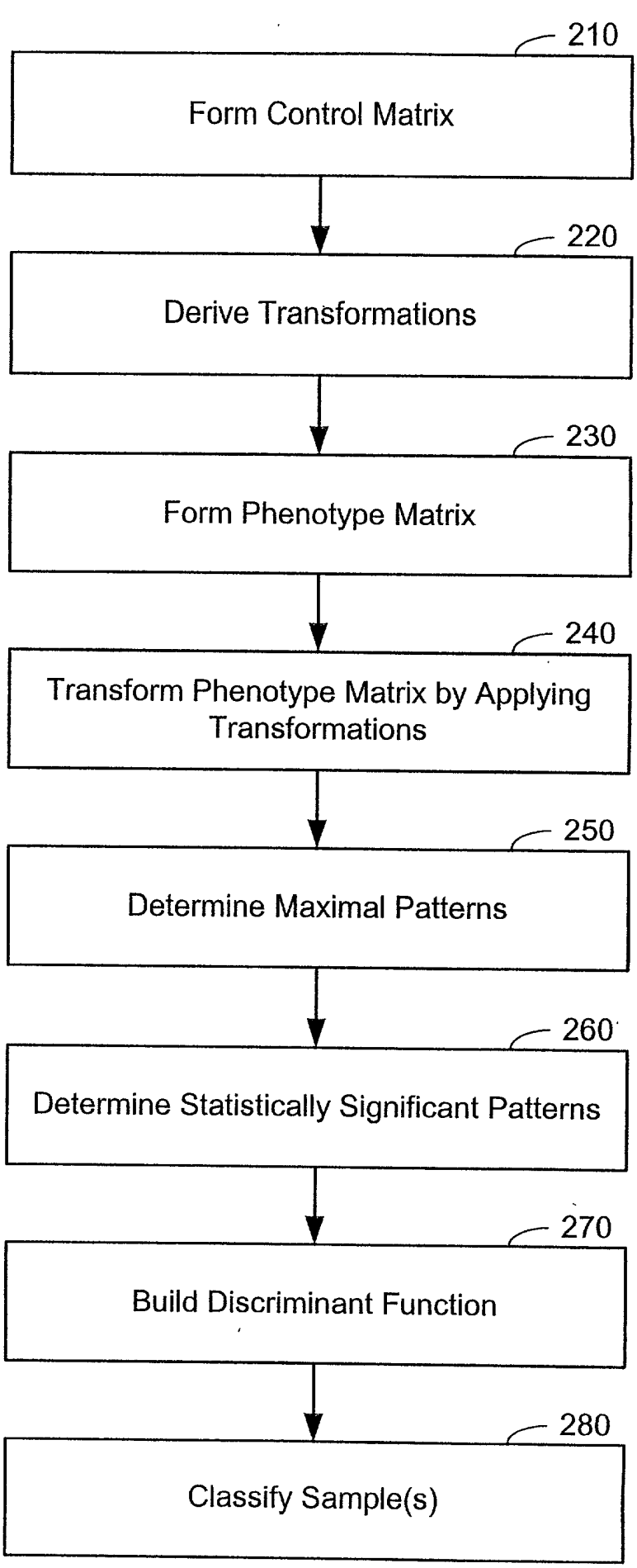
200
210
Form Control Matrix
220
Derive Transformations
230
Form Phenotype Matrix
240
Transform Phenotype Matrix by Applying Transformations
250
Determine Maximal Patterns
260
Determine Statistically Significant Patterns
270
Build Discriminant Function
280
Classify Sample(s)

FIG. 2

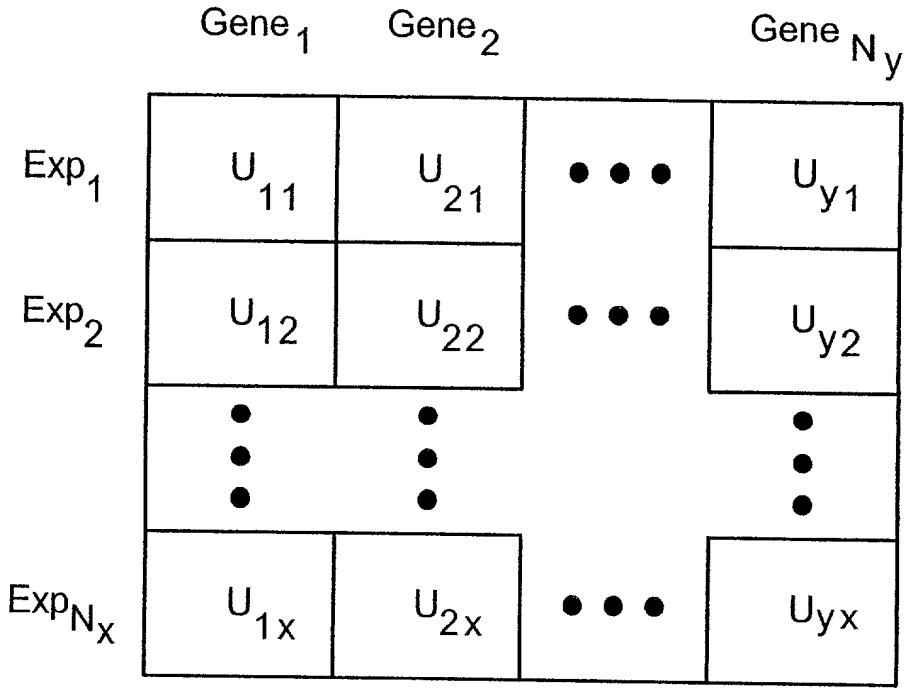
Gene 1
Gene 2
Gene Ny
Exp1
Exp2
ExpNx
U11
U21
Uy1
U12
U22
Uy2
U1x
U2x
Uyx

FIG. 3

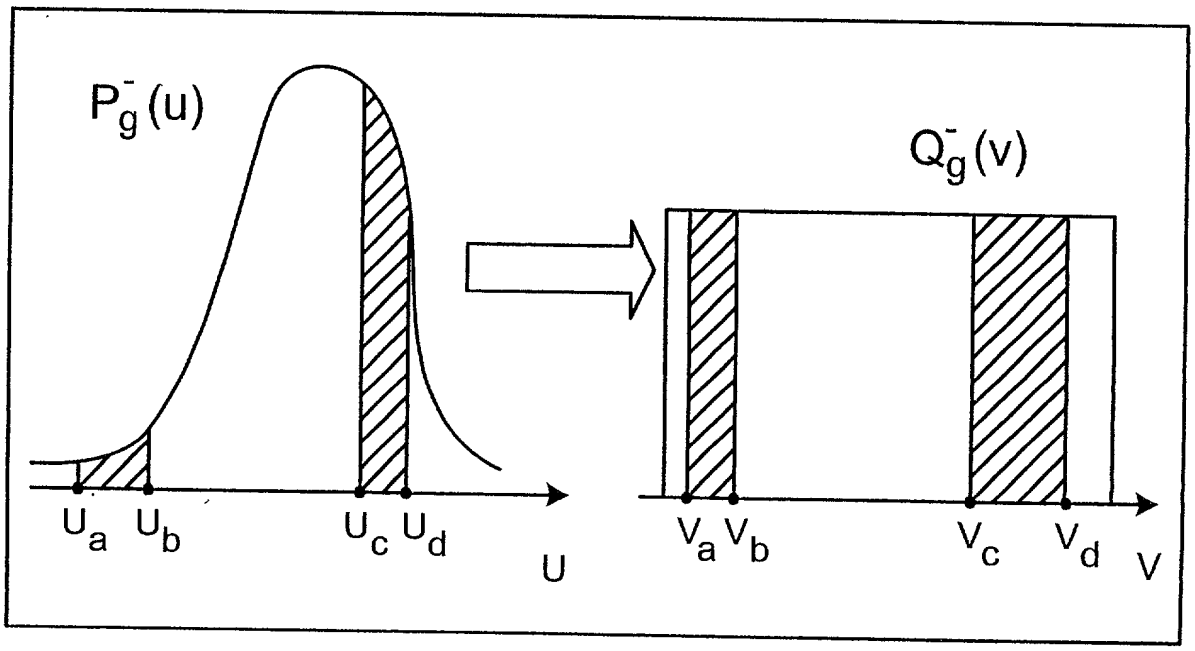
P-g(u)
Q-g(v)
Ua
Ub
Uc
Ud
U
Va
Vb
Vc
Vd
V

FIG. 4

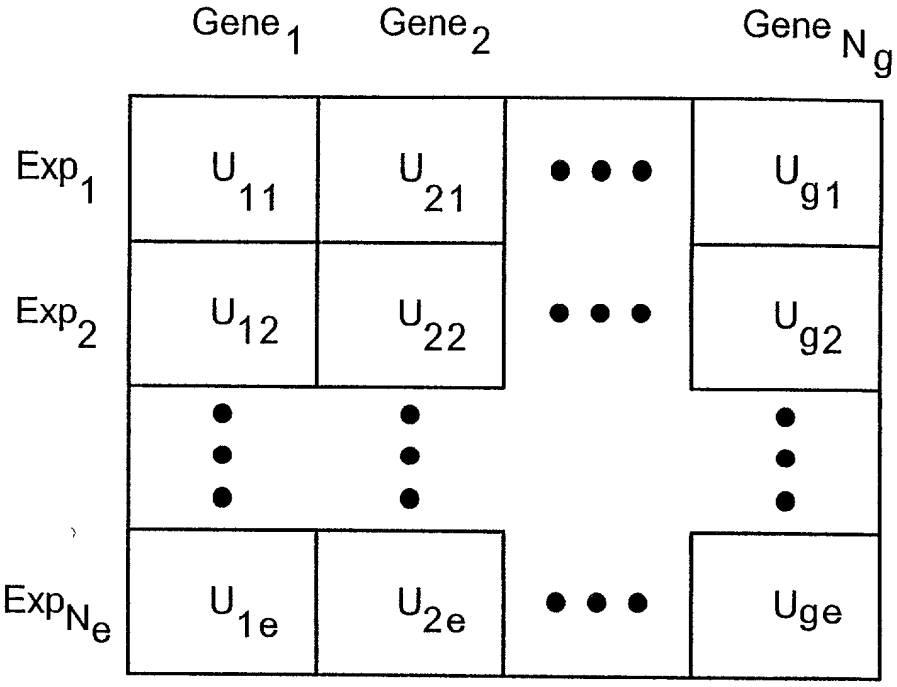

FIG. 5

	Gene$_1$	Gene$_2$	Gene$_3$	Gene$_4$	Gene$_5$
Exp$_1$	0.1	0.3	0.6	0.7	0.8
Exp$_2$	0.1	0.2	0.5	0.7	0.5
Exp$_3$	0.1	0.2	0.1	0.9	0.6
Exp$_4$	0.1	0.2	0.5	0.6	0.6

N_e

N_g

FIG. 6

$$V_{G,E} = \begin{bmatrix} 0.1 & 0.6 & 0.7 \\ 0.1 & 0.5 & 0.7 \\ 0.1 & 0.5 & 0.6 \end{bmatrix}$$

FIG. 7

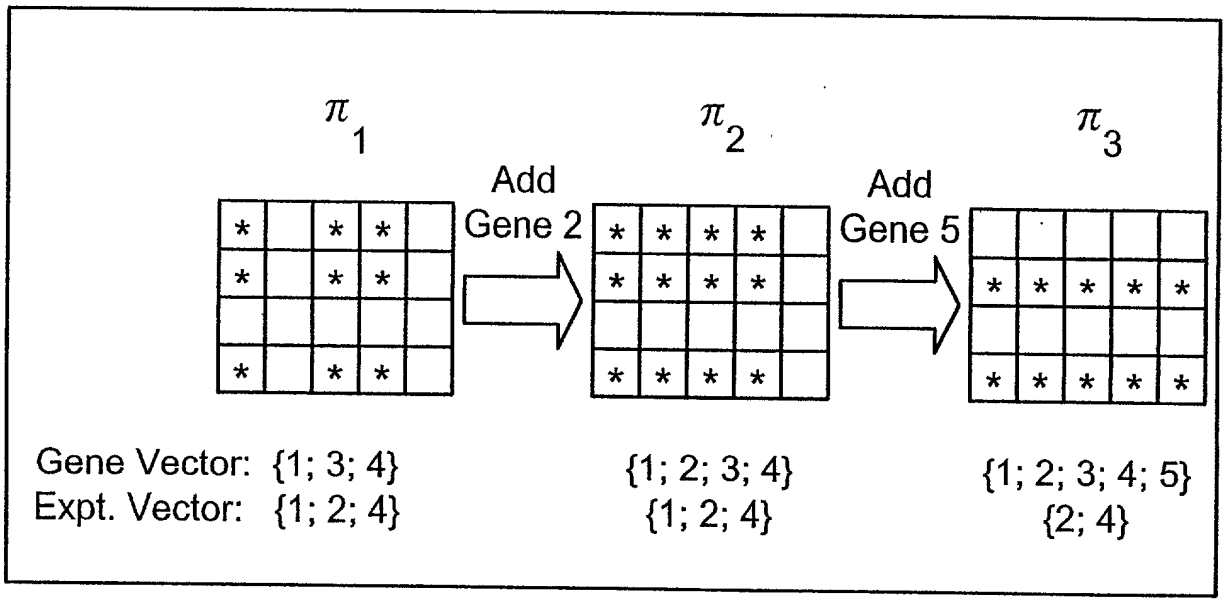

FIG. 8

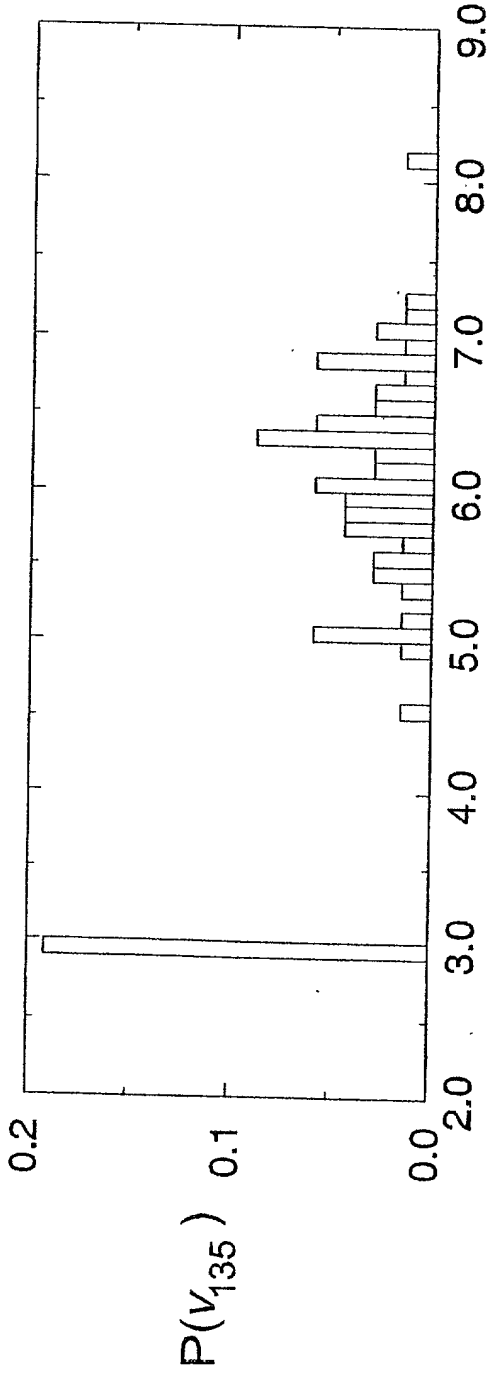

FIG. 9

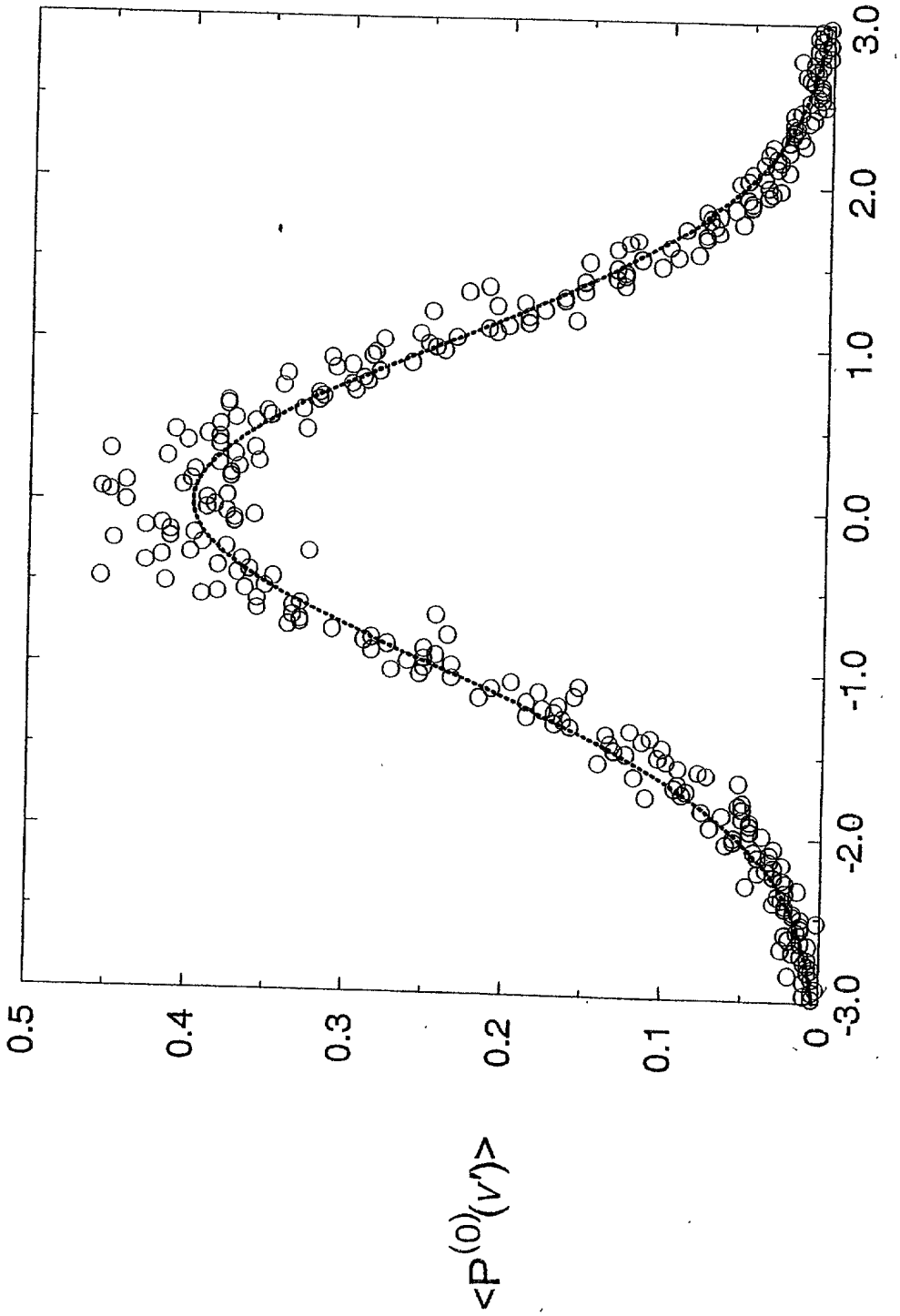

FIG. 10

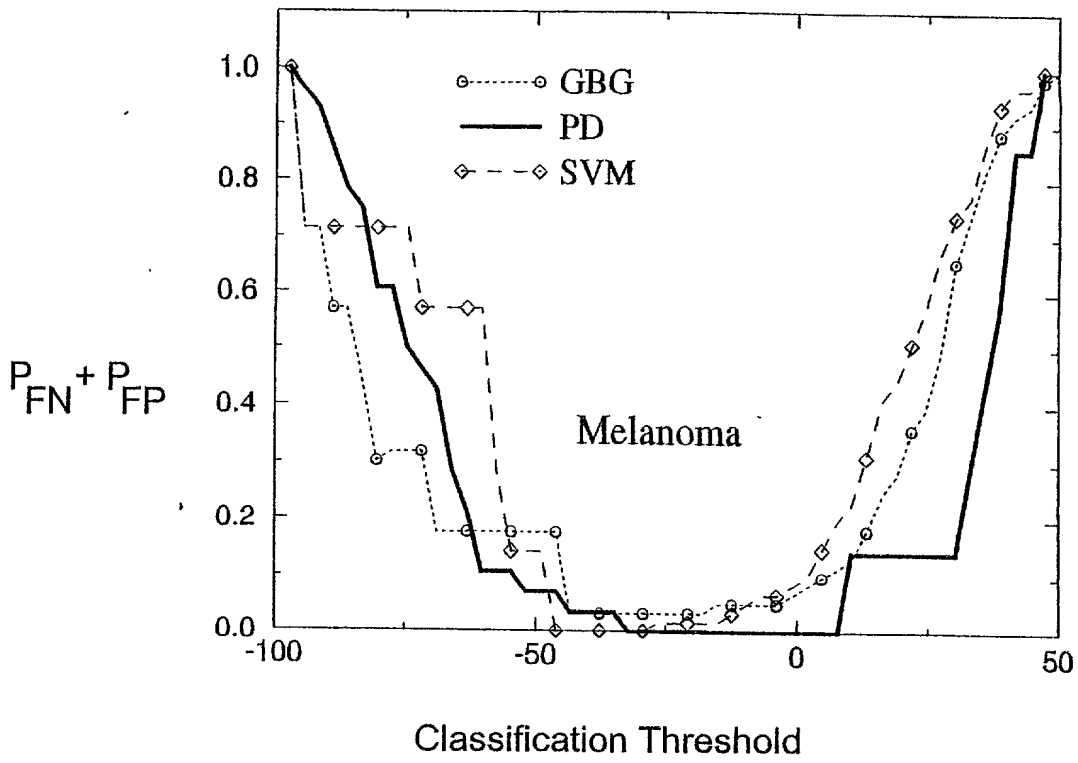
GBG
PD
SVM
Melanoma
$P_{FN} + P_{FP}$
1.0
0.8
0.6
0.4
0.2
0.0
-100
-50
0
50
Classification Threshold

FIG. 11

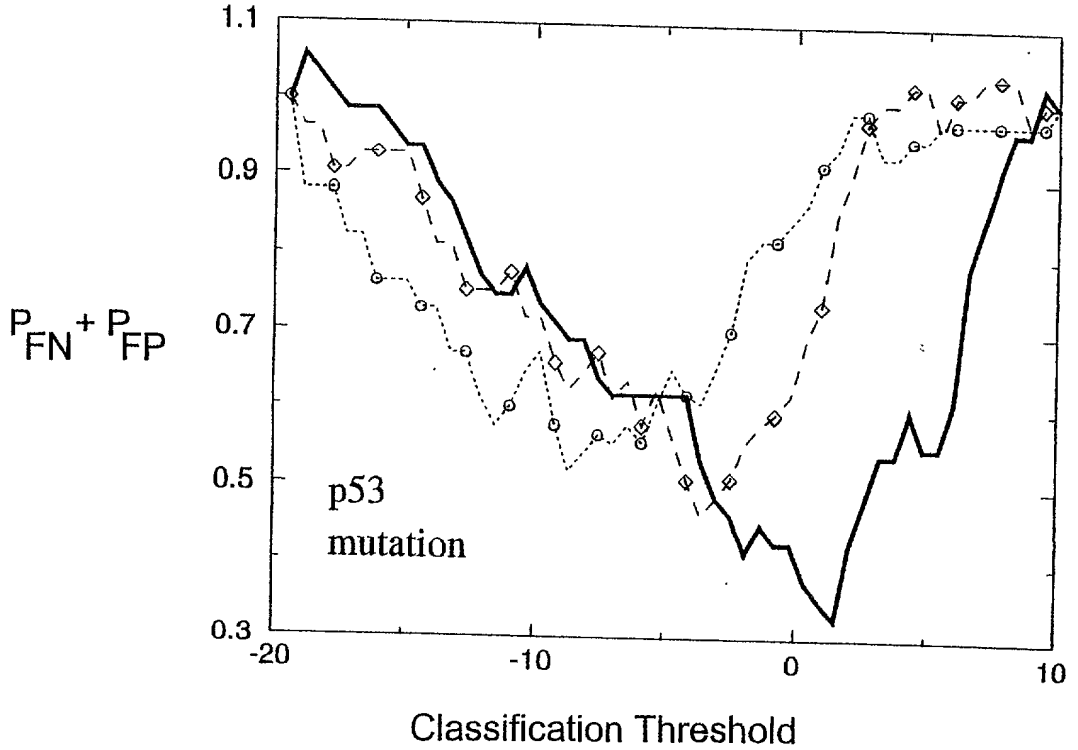
p53
mutation
$P_{FN} + P_{FP}$
1.1
0.9
0.7
0.5
0.3
-20
-10
0
10
Classification Threshold

FIG.12

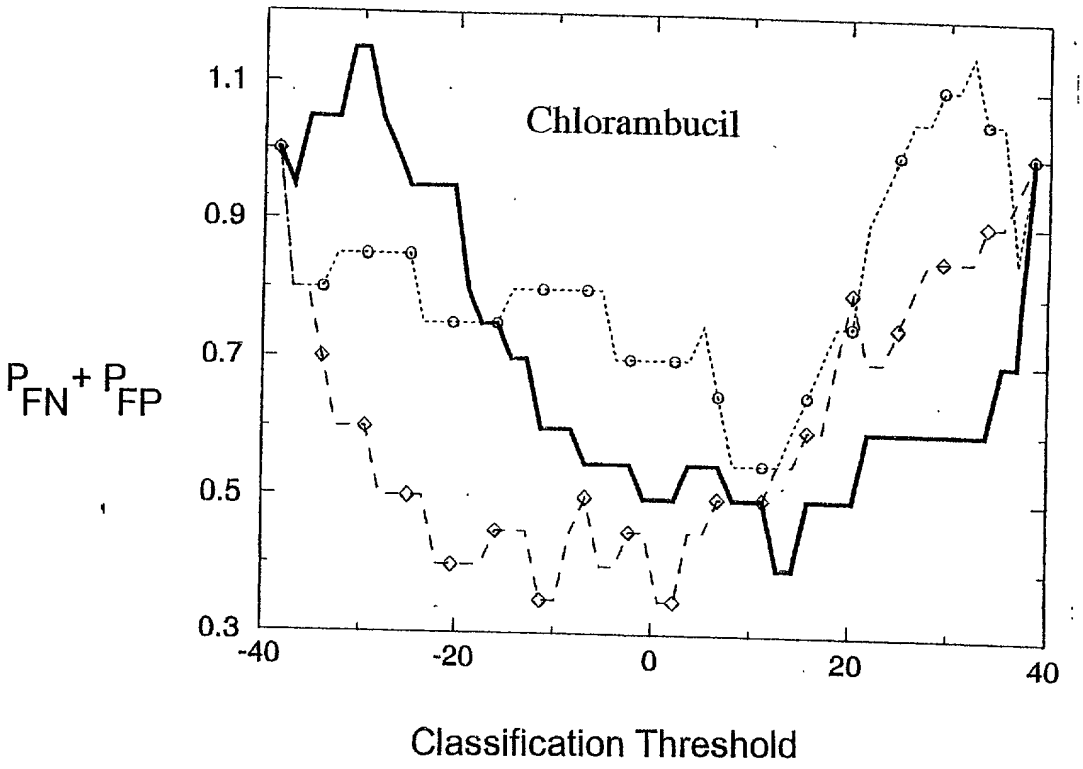
Chlorambucil
$P_{FN} + P_{FP}$
1.1
0.9
0.7
0.5
0.3
-40
-20
0
20
40
Classification Threshold

FIG. 13

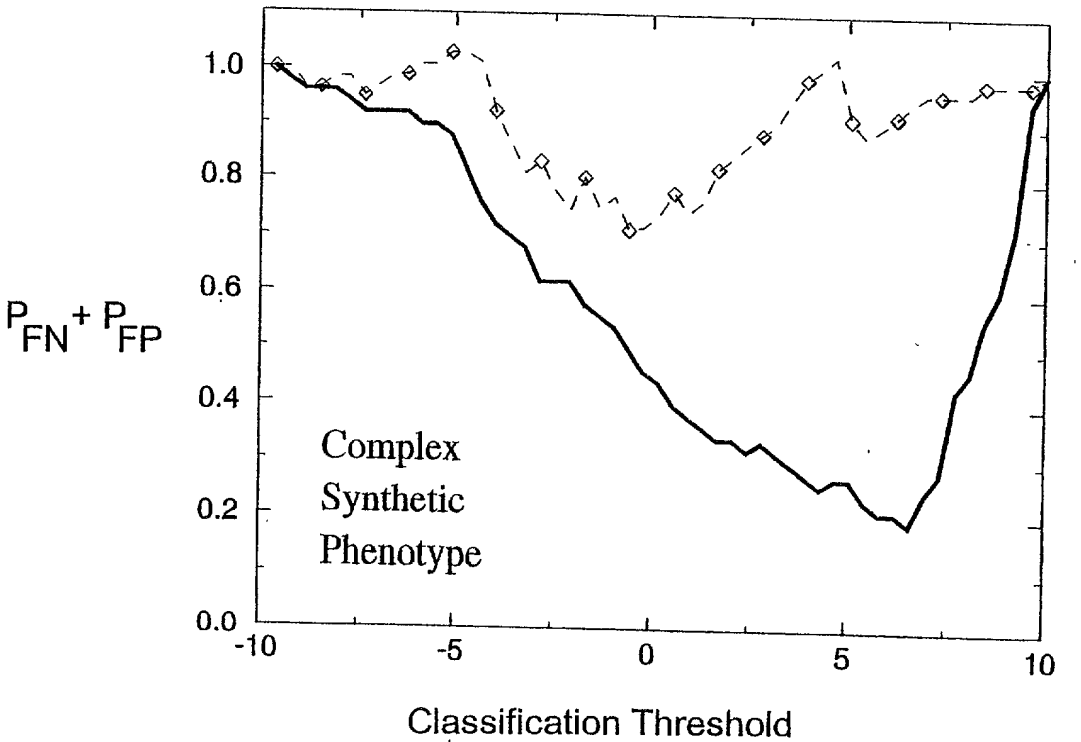
Complex
Synthetic
Phenotype
$P_{FN} + P_{FP}$
1.0
0.8
0.6
0.4
0.2
0.0
-10
-5
0
5
10
Classification Threshold

FIG.14

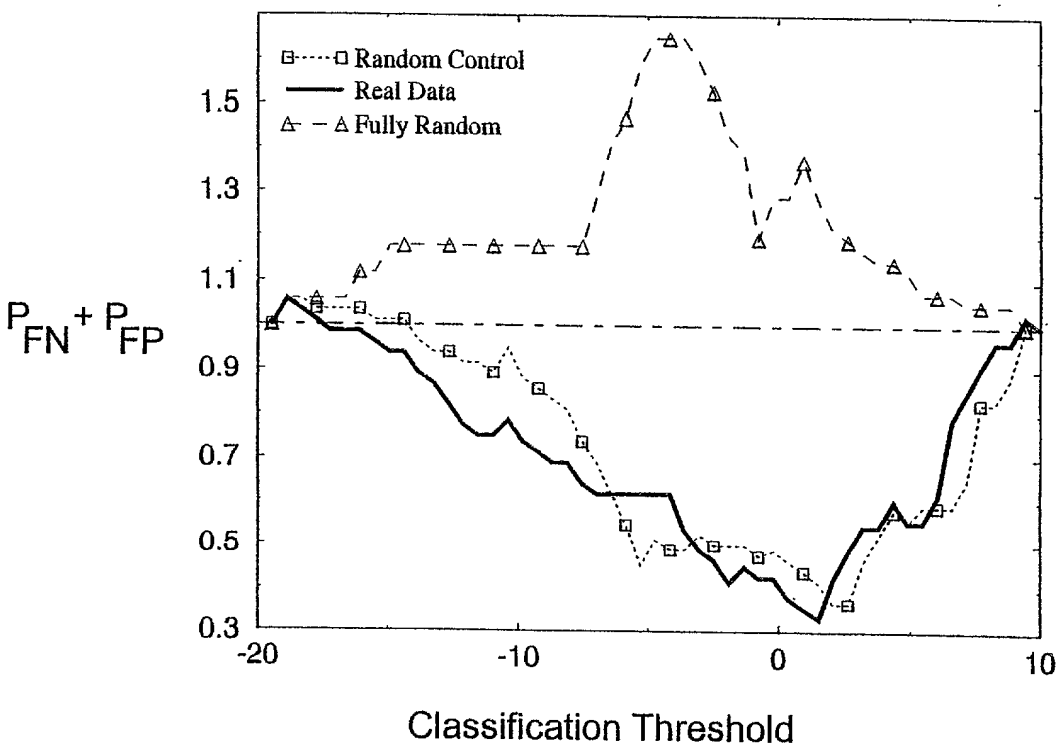
Random Control
Real Data
Fully Random
1.5
1.3
1.1
0.9
0.7
0.5
0.3
-20
-10
0
10
$P_{FN} + P_{FP}$
Classification Threshold

FIG. 15